

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 101725,037
Source: JFWB0
Date Processed by STIC: 10/18/04

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IFWO

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/725,037

DATE: 10/18/2004
 TIME: 10:28:10

Input Set : A:\78031566.app
 Output Set: N:\CRF4\10182004\J725037.raw

3 <110> APPLICANT: ZOLLER, MARK
 4 LI, XIAODONG
 5 STASZEWSKI, LENA
 6 O'CONNELL, SHAWN
 7 ZOZULYA, SERGEY
 8 ADLER, JON
 9 XU, HONG
 10 ECHEVERRI, FERNANDO
 12 <120> TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
 13 THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
 14 IDENTIFICATION OF TASTE COMPOUNDS
 16 <130> FILE REFERENCE: 078003-0291566
 --> 18 <140> CURRENT APPLICATION NUMBER: US/10/725,037
 --> 19 <141> CURRENT FILING DATE: 2003-12-02
 21 <150> PRIOR APPLICATION NUMBER: 60/300,434
 22 <151> PRIOR FILING DATE: 2001-06-26
 24 <150> PRIOR APPLICATION NUMBER: 60/304,749
 25 <151> PRIOR FILING DATE: 2001-07-13
 27 <150> PRIOR APPLICATION NUMBER: 60/310,493
 28 <151> PRIOR FILING DATE: 2001-08-08
 30 <150> PRIOR APPLICATION NUMBER: 60/331,771
 31 <151> PRIOR FILING DATE: 2001-11-21
 33 <150> PRIOR APPLICATION NUMBER: 60/339,472
 34 <151> PRIOR FILING DATE: 2001-12-14
 36 <150> PRIOR APPLICATION NUMBER: 60/372,090
 37 <151> PRIOR FILING DATE: 2002-04-15
 39 <150> PRIOR APPLICATION NUMBER: 60/374,143
 40 <151> PRIOR FILING DATE: 2002-04-22
 42 <160> NUMBER OF SEQ ID NOS: 19
 44 <170> SOFTWARE: PatentIn Ver. 2.1
 46 <210> SEQ ID NO: 1
 47 <211> LENGTH: 5
 48 <212> TYPE: PRT
 49 <213> ORGANISM: Artificial Sequence
 51 <220> FEATURE:
 52 <223> OTHER INFORMATION: Description of Artificial Sequence: PDZIP sequence
 54 <400> SEQUENCE: 1
 55 Ser Val Ser Thr Trp
 56 1 5
 59 <210> SEQ ID NO: 2
 60 <211> LENGTH: 14
 61 <212> TYPE: PRT
 62 <213> ORGANISM: Artificial Sequence

(P5,6)

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64 <220> FEATURE:
65 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
66 sequence
68 <220> FEATURE:
69 <221> NAME/KEY: MOD_RES
70 <222> LOCATION: (1)
71 <223> OTHER INFORMATION: Thr or Arg
73 <220> FEATURE:
74 <221> NAME/KEY: MOD_RES
75 <222> LOCATION: (3)
76 <223> OTHER INFORMATION: Phe or Leu
78 <220> FEATURE:
79 <221> NAME/KEY: MOD_RES
80 <222> LOCATION: (4)
81 <223> OTHER INFORMATION: Arg, Gln or Pro
83 <220> FEATURE:
84 <221> NAME/KEY: MOD_RES
85 <222> LOCATION: (6)
86 <223> OTHER INFORMATION: Arg or Thr
88 <220> FEATURE:
89 <221> NAME/KEY: MOD_RES
90 <222> LOCATION: (7)
91 <223> OTHER INFORMATION: Ser, Pro or Val
93 <220> FEATURE:
94 <221> NAME/KEY: MOD_RES
95 <222> LOCATION: (8)
96 <223> OTHER INFORMATION: Val, Glu, Arg, Lys or Thr
98 <220> FEATURE:
99 <221> NAME/KEY: MOD_RES
100 <222> LOCATION: (11)
101 <223> OTHER INFORMATION: Ala or Glu
103 <220> FEATURE:
104 <221> NAME/KEY: MOD_RES
105 <222> LOCATION: (12)
106 <223> OTHER INFORMATION: Trp or Leu
108 <220> FEATURE:
109 <221> NAME/KEY: MOD_RES
110 <222> LOCATION: (13)
111 <223> OTHER INFORMATION: Arg, His or Gly
113 <400> SEQUENCE: 2
-> 114 Xaa Cys Xaa Xaa Arg Xaa Xaa Xaa Phe Leu Xaa Xaa Xaa Glu
115 1 5 10
118 <210> SEQ ID NO: 3
119 <211> LENGTH: 15
120 <212> TYPE: PRT
121 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
125 sequence

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127 <220> FEATURE:
128 <221> NAME/KEY: MOD_RES
129 <222> LOCATION: (1)
130 <223> OTHER INFORMATION: Leu or Gln
132 <220> FEATURE:
133 <221> NAME/KEY: MOD_RES
134 <222> LOCATION: (3)
135 <223> OTHER INFORMATION: Glu, Gly or Thr
137 <220> FEATURE:
138 <221> NAME/KEY: MOD_RES
139 <222> LOCATION: (4)
140 <223> OTHER INFORMATION: Asn, Arg or Cys
142 <220> FEATURE:
143 <221> NAME/KEY: MOD_RES
144 <222> LOCATION: (7)
145 <223> OTHER INFORMATION: Arg or Glu
147 <220> FEATURE:
148 <221> NAME/KEY: MOD_RES
149 <222> LOCATION: (9)
150 <223> OTHER INFORMATION: Arg or Lys
152 <220> FEATURE:
153 <221> NAME/KEY: MOD_RES
154 <222> LOCATION: (10)
155 <223> OTHER INFORMATION: Cys, Gly or Phe
157 <220> FEATURE:
158 <221> NAME/KEY: MOD_RES
159 <222> LOCATION: (11)
160 <223> OTHER INFORMATION: Val, Leu or Ile
162 <220> FEATURE:
163 <221> NAME/KEY: MOD_RES
164 <222> LOCATION: (13)
165 <223> OTHER INFORMATION: Phe or Leu
167 <220> FEATURE:
168 <221> NAME/KEY: MOD_RES
169 <222> LOCATION: (14)
170 <223> OTHER INFORMATION: Ala or Ser
172 <220> FEATURE:
173 <221> NAME/KEY: MOD_RES
174 <222> LOCATION: (15)
175 <223> OTHER INFORMATION: Met or Leu
177 <400> SEQUENCE: 3
-> 178 Xaa Pro Xaa Xaa Tyr Asn Xaa Ala Xaa Xaa Xaa Thr Xaa Xaa Xaa
179 1 5 10 15
182 <210> SEQ ID NO: 4
183 <211> LENGTH: 858
184 <212> TYPE: PRT
185 <213> ORGANISM: Rattus sp.
187 <400> SEQUENCE: 4
188 Met Pro Gly Leu Ala Ile Leu Gly Leu Ser Leu Ala Ala Phe Leu Glu

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189	1	5	10	15												
191	Leu	Gly	Met	Gly	Ser	Ser	Leu	Cys	Leu	Ser	Gln	Gln	Phe	Lys	Ala	Gln
192			20				25						30			
194	Gly	Asp	Tyr	Ile	Leu	Gly	Gly	Leu	Phe	Pro	Leu	Gly	Thr	Thr	Glu	Glu
195							35						45			
197	Ala	Thr	Leu	Asn	Gln	Arg	Thr	Gln	Pro	Asn	Gly	Ile	Leu	Cys	Thr	Arg
198							50						60			
200	Phe	Ser	Pro	Leu	Gly	Leu	Phe	Leu	Ala	Met	Ala	Met	Lys	Met	Ala	Val
201							65						75			80
203	Glu	Glu	Ile	Asn	Asn	Gly	Ser	Ala	Leu	Leu	Pro	Gly	Leu	Arg	Leu	Gly
204							85						90			95
206	Tyr	Asp	Leu	Phe	Asp	Thr	Cys	Ser	Glu	Pro	Val	Val	Thr	Met	Lys	Pro
207							100						105			110
209	Ser	Leu	Met	Phe	Met	Ala	Lys	Val	Gly	Ser	Gln	Ser	Ile	Ala	Ala	Tyr
210							115						120			125
212	Cys	Asn	Tyr	Thr	Gln	Tyr	Gln	Pro	Arg	Val	Leu	Ala	Val	Ile	Gly	Pro
213							130						135			140
215	His	Ser	Ser	Glu	Leu	Ala	Leu	Ile	Thr	Gly	Lys	Phe	Phe	Ser	Phe	Phe
216							145						150			160
218	Leu	Met	Pro	Gln	Val	Ser	Tyr	Ser	Ala	Ser	Met	Asp	Arg	Leu	Ser	Asp
219							165						170			175
221	Arg	Glu	Thr	Phe	Pro	Ser	Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Arg	Val
222							180						185			190
224	Gln	Leu	Gln	Ala	Val	Val	Thr	Leu	Leu	Gln	Asn	Phe	Ser	Trp	Asn	Trp
225							195						200			205
227	Val	Ala	Ala	Leu	Gly	Ser	Asp	Asp	Asp	Tyr	Gly	Arg	Glu	Gly	Leu	Ser
228							210						215			220
230	Ile	Phe	Ser	Gly	Leu	Ala	Asn	Ser	Arg	Gly	Ile	Cys	Ile	Ala	His	Glu
231							225						230			240
233	Gly	Leu	Val	Pro	Gln	His	Asp	Thr	Ser	Gly	Gln	Gln	Leu	Gly	Lys	Val
234							245						250			255
236	Val	Asp	Val	Leu	Arg	Gln	Val	Asn	Gln	Ser	Lys	Val	Gln	Val	Val	Val
237							260						265			270
239	Leu	Phe	Ala	Ser	Ala	Arg	Ala	Val	Tyr	Ser	Leu	Phe	Ser	Tyr	Ser	Ile
240							275						280			285
242	Leu	His	Asp	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ser	Trp	Leu
243							290						295			300
245	Thr	Ser	Asp	Leu	Val	Met	Thr	Leu	Pro	Asn	Ile	Ala	Arg	Val	Gly	Thr
246							305						310			320
248	Val	Leu	Gly	Phe	Leu	Gln	Arg	Gly	Ala	Leu	Leu	Pro	Glu	Phe	Ser	His
249							325						330			335
251	Tyr	Val	Glu	Thr	Arg	Leu	Ala	Leu	Ala	Ala	Asp	Pro	Thr	Phe	Cys	Ala
252							340						345			350
254	Ser	Leu	Lys	Ala	Glu	Leu	Asp	Leu	Glu	Glu	Arg	Val	Met	Gly	Pro	Arg
255							355						360			365
257	Cys	Ser	Gln	Cys	Asp	Tyr	Ile	Met	Leu	Gln	Asn	Leu	Ser	Ser	Gly	Leu
258							370						375			380
260	Met	Gln	Asn	Leu	Ser	Ala	Gly	Gln	Leu	His	His	Gln	Ile	Phe	Ala	Thr
261							385						390			400

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263 Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln
 264 405 410 415
 266 Cys Asn Val Ser His Cys His Thr Ser Glu Pro Val Gln Pro Trp Gln
 267 420 425 430
 269 Leu Leu Glu Asn Met Tyr Asn Met Ser Phe Arg Ala Arg Asp Leu Thr
 270 435 440 445
 272 Leu Gln Phe Asp Ala Lys Gly Ser Val Asp Met Glu Tyr Asp Leu Lys
 273 450 455 460
 275 Met Trp Val Trp Gln Ser Pro Thr Pro Val Leu His Thr Val Gly Thr
 276 465 470 475 480
 278 Phe Asn Gly Thr Leu Gln Leu Gln His Ser Lys Met Tyr Trp Pro Gly
 279 485 490 495
 281 Asn Gln Val Pro Val Ser Gln Cys Ser Arg Gln Cys Lys Asp Gly Gln
 282 500 505 510
 284 Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp
 285 515 520 525
 287 Cys Lys Ala Gly Ser Tyr Arg Lys His Pro Asp Asp Phe Thr Cys Thr
 288 530 535 540
 290 Pro Cys Gly Lys Asp Gln Trp Ser Pro Glu Lys Ser Thr Thr Cys Leu
 291 545 550 555 560
 293 Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Ala Val Leu Ser
 294 565 570 575
 296 Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Thr Leu Ala Ala Leu
 297 580 585 590
 299 Gly Leu Phe Val His Tyr Trp Asp Ser Pro Leu Val Gln Ala Ser Gly
 300 595 600 605
 302 Gly Ser Leu Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu
 303 610 615 620
 305 Ser Val Leu Leu Phe Pro Gly Arg Pro Arg Ser Ala Ser Cys Leu Ala
 306 625 630 635 640
 308 Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu
 309 645 650 655
 311 Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser
 312 660 665 670
 314 Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Pro Trp Ala Trp Leu
 315 675 680 685
 317 Val Val Leu Leu Ala Thr Leu Val Glu Ala Ala Leu Cys Ala Trp Tyr
 318 690 695 700
 320 Leu Met Ala Phe Pro Pro Glu Val Val Thr Asp Trp Gln Val Leu Pro
 321 705 710 715 720
 323 Thr Glu Val Leu Glu His Cys Arg Met Arg Ser Trp Val Ser Leu Gly
 324 725 730 735
 326 Leu Val His Ile Thr Asn Ala Val Leu Ala Phe Leu Cys Phe Leu Gly
 327 740 745 750
 329 Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly
 330 755 760 765
 332 Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Ile Trp Val Ser Phe Val
 333 770 775 780
 335 Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/18/2004
PATENT APPLICATION: US/10/725,037 TIME: 10:28:11

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 1,3,4,6,7,8,11,12,13

Seq#:3; Xaa Pos. 1,2,4,7,9,10,11,13,14,15

Seq#:13; Xaa Pos. 120,121

Seq#:15; Xaa Pos. 8,15,59,62,76,117,128,136,168,173,175,176,203,226

VERIFICATION SUMMARY

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L:18 M:270 C: Current Application Number differs, Replaced Current Application Number
L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:1121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:112
L:1259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
M:341 Repeated in SeqNo=15